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Baldwin, J., Barna, N. Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funce, K., Gage, D., Howland, J. Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwald, J., McEwald, M., McEwald, J., Waldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Stangerhomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Whitel, M., Wold, M., Wheeler, J., Wu, X., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (27-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, NA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. 6 Green, P. (1996-1997) Green, Washington.edu/RW/RepeatMasker.html.

* Sequencing reads that have not been assembled into anothins. Runs of N are used to separate the reads antitary. Low-pass Sequence sampling is useful for overlap relationships among clones to be deduced.

* Vill be sequenced to completion. In the event that the record is undared that this clone.
                                                                                                                                                                                                                                                                                                               ACU12422 53967 bp DNA HTG 27-OCT-1999
HOMO Sapiens chromosome 15 clone 141_E_4 map 15, LOW-PASS SEQUENCE
AC012422
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin!; Hominidae; Homo. I to 53967) El Dases I to 53967) Elren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone 141_E_4
                                                                                                 ö
                                                          Length 250;
                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             722: contig of 722 bp in length
gap of unknown length
1504: contig of 782 bp in length
gap of unknown length
2265: contig of 761 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
of 760 bp in length
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of 766 bp in length
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of 817 bp in length
                                    Ouery Match
1.1%; Score 98; DB 13; L.
Best Local Similarity 100.0%; Pred. No. 4e-43;
Matches 98; Conservative 0; Mismatches 0;
                                                                                                                                                                                  gap of contig
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3791: contig
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HTG; HTGS_PHASE0.
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Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
7634 taggettaaacetygaatetacaagecaaaagteeeteeetgeetgaggeagtaeeet 7693
                                                                                                     7753
                     04-JAN-1996
                                                                      Prepared with primer pairs derived from T65388--Merck/UniEST.
Location/Qualifiers
1. 250
/Organism-"Homo sapiens"
(57 197
Lbind 67. 188
                                                                                                                                            94 degrees C for 15 seconds
62 degrees C for 23 seconds
72 degrees C for 30 seconds
30
Perkin Elmer 9600
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Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          initial incubation: 94 degrees C for 90 seconds
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each 1 um
each 200 um
0.05 units/ul
10 ul
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Stanford Human Genome Center (SHGC)
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Primer B: GGACGGACCAGCATCTGG
STS size: 131
PCR Profile:
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Email: myers@shgc.stanford.edu
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50 mM
20 mM
8.3
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48 c 43 g
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Annealing:
Polymerization:
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Thermal Cycler;
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Total Vol;
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Template: Primer: dNTPs:

Protocol

KCl: Tris-HCl:

85 8

primer\_bind primer\_bind

BASE COUNT

Source

FEATURES

MgC12:

Buffer:

Myers, R.M. Unpublished (1995)

AUTHORS JOURNAL COMMENT REFERENCE

Homo sapiens

G15289

RESULT 11 G15289/c

LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

unknown length

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G43056
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (basea I to 23)
I shii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H., Hori, M., Fidanza, V., Alder, H. and Croce, C.M.
The FEZI gene at chromosome 8p22 encodes a leucine-zipper protein, and its expression is altered in multiple human tumors proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 231)
National Parties, Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,
Mori, M., Fidanza, V., Alder, H. and Croce, C.M.
Direct Submission
                                                                                                                                                                   AF123652 231 bp mRNA PRI 07-APR-1999
Homo sapiens clone E16T8 FEZ1 (FEZ1) mRNA, alternatively spliced,
complete cds.
                             112 tegeagtacaagetgegeaagteeteecaceteaagaageteaaceggtatteegaeggg 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-3AN-1999) Immunology/Microbiology, Kimmel Cancer Institute, 2335 10th street, Philadelphia, PA 19107, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
1 TAGGCTTANACCTGGNATCTACAAGACCAAAAGTCCCTCCCTGCCTGAGGGCAGTACCCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                     1.8%; Score 162; DB 40; Length 231; 100.0%; Pred. No. 6e-79; 1.1ve 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/chromosome="8"
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Matches 162; Conservative
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/organism="Homo sapiens"
/db_xref="texon:9606"
/map="41.70 cR from top of Chr8 linkage group"
/clone_lib="Human THudson SANGER"
/note="human STS created from EST in the Sanger database"
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                                                                                                                                                                  Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 172)

Rang, D.G., Fan, J.B., Siao, C.J., Berno, A., Young, P., Sapolsky, R., Ghandour, G., Perkins, N., Winchester, E., Spencer, J., Kruglyak, L., Stein, L., Hale, L., Topaloglou, T., Hubbell, E., Robinson, E., Mittmann, M., Morris, M.S., Shen, N., Kilburn, D., Rioux, J., Nusbaum, C., Rozen, S., Hudson, T.J., Lipshutz, R., Chee, M. and
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G43056 172 bp DNA STS 27-JAN-1999 WIAF-1517-STS Human THudson SANGER Homo sapiens STS genomic,
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Pred. No. 5.3e-56;
0; Mismatches 1;
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each 5 pM
4 nM
: 0.5 U
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Primer A: TAGGCTPAAACCTGGAATCTAC
Primer B: CTCACTGGGAGGAAAAC
STS Size: 172
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58 c 3
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Best Local Similarity 99.4%;
Matches 171; Conservative
                                                sequence tagged site.
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G43056.1 GI:4191973
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PCR Profile:
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Gapop 60.0 , Gapext 60.0
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-5616.025 Million cell updates/sec
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AF123653 9108 bp I
Homo sapiens FEZI (FEZI)
AF123653
AF123653:1 GI:4572463
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                           complete
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G43056 WIAF-1517-5

G15289 human STS

G1012422 Homo sapi

AC0011963 Homo sapi

AC0011963 Homo sapi

AC0011971 Homo sapi

AC0011971 Homo sapi

AC003569 Homo sapi

AC003569 Homo sapi

AC0035749 Human DNA

AC004707 Homo sapien

AL035249 Human DNA

AC004707 Homo sapien

AL045547 Homo sapi

AC009833 Homo sapi

AC009833 Homo sapi

AC0101407 Homo sapi

AC0101407 Homo sapi

AC011407 Homo sapi

AC005017 Homo sapi

AC007092 H.sapiens f

AJ009617 Homo sapi

AC007092 Homo sapi

AC007092 Homo sapi
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AL121971 Homo sapien
295152 Homo sapien
AC006538 Homo sapi.
AC007375 Homo sapi.
AC003682 Homo sapi.
AC008569 Homo sapi.
AC009280 Homo sapi.
AL121885 Homo sapi.
AC006966 Homo sapi.
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07-APR-1999

AF123658 Homo sap AF123654 Homo sap G60003 SHGC-13079

AF123653 Homo sap AF123659 Homo sap AF123656 Homo sap AF123655 Homo AF123657 Homo

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G43056
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/product="rez1"
/protein_id="aAD23833.1"
/protein_id="AAD23833.1"
/cd_xref="c1:4572452"
/cd_xr
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Eukaryota, Hetazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (basea 1 to 231)
15h1i, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,
Mori, M., Fidanza, V., Alder, H. and Croce, C.M.
The FE21 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 231)
Ishil,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Ishil,H., Baffa,R., Alder,H. and Croce,C.M.
Divort, Submission
Submisted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 2335 10th street, Philadelphia, PA 19107, USA
Location/Qualifiers
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Homo sapiens clone E16TB FE21 (FE21) mRNA, alternatively spliced,
complete cds.
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1 INGGCTTAMACCIGGNATCTACAAGCCAMAMGTCCCTCCCTGCCTGAGGGCAGIACCCIC 60
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                                                                                                                                                                      Query Match
1.8%; Score 162; DB 40; Length 231;
Best Local Similarity 100.0%; Pred. No. 6e-79;
Matches 162; Conservative 0; Mismatches 0; Indels
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
/map="42.70 cR from top of Chr8 linkage group"
/clone_lib-"Human THudson SANGER"
/note-"human STS created from EST in the Sanger database"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermal Cycler: custom built by IAS, Costar, Cambridge MA
                                                                                                                                                                                                                  l (bases 1 to 172)
Wang, D.G., Fan, J.B., Slao, C.J., Berno, A., Young, P., Sapolsky, R., Mang, D.G., Fan, J.B., Slao, C.J., Berno, A., Spencer, J., Kruglyak, L., Stain, L., Hale, L., Topaloglou, T., Hubbell, E., Robinson, E., Mittmann, M., Morris, M.S., Shen, N., Kilburn, D., Rioux, J., Nusbaum, C., Rozen, S., Hudson, T.J., Lipshutz, R., Chee, M. and
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                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172)
G43056 172 bp DNA STS 27-JAN-1999 WIAP-1517-STS Human THudson SANGER Homo sapiens STS genomic,
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Pred. No. 5.3e-56;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Thomas Hidson Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research S Cambridge Center, Cambridge MA 02142 USA 191: 617 252 1900
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each 5 pM
4 nM
4 se: 0.5 U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: thudson@genome.wi.mit.edu
Primer A: TAGGCTTAAACCTGGAATCTAC
Primer B: CTCACTGGGAGGAAAAC
STS size: 172
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(155. .172)
58 c 34 q
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Best Local Similarity 99.4%;
Matches 171; Conservative (
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Total Vol:
                                                  sequence tagged site.
                                                                                      GI:4191973
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Gelatin:
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27-OCT-1999 LOW-PASS SEQUENCE

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FEATURES
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G15289/c
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                                                                                                                                                                  Prepared with primer pairs derived Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                      Protoco!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer A: TGCCACAAATAGTTTACATGGC
Primer B: GGACGGACCAGCATCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STS size:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Richard M. Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primate, Catarrhini; Hominidae; Homo.

1 (bases 1 to 250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
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STS sequence; primer; sequence tagged site.
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KCl:
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STS SHGC-15950.
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                                                                                                          /organism="Homo sapiens" 67. 197 67. 88
                                                                                                                                                                                                                                                                                                                              Tag Polymerase:
Total Vol:
                                                                                       complement(180.
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Polymerization:
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each 1 uM
each 200 uM
: 0.05 units/ul
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50 mx
20 mx
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62 degrees C
72 degrees C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              RS Biren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkly, L., Boukhgalter, B., Baldwin, J., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cocke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marguis, N., Kernan, K., McLaughlin, J., Meddrim, J., Morman, C. H., O'Connor, T., O'Donnell, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Direct Submission
                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html.
NOTE: This record contains 70 individual
sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 GTTTTTATTTATGAATAAAGAATGCCATTTCTCACGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (27-0CT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P_(1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 53967)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 15, clone 141_E_4
                                                                                                                                                                                               be preserved.
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                                                                                                                                                                                                           is updated, the accession
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1504: gap of unknown length
contig of 782 bp in length
gap of unknown length
2265: contig of 761 bp in length
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gap of unknown length contig of 817 bp in length
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Pred. No. 4e-43;
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